

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Communi, Didier
Piroton, Sabine
Parmentier, Marc
Boeynaems, Jean-Marie

(ii) TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE
ENCODING SAID RECEPTOR

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDANCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
(B) STREET: 501 West Broadway
(C) CITY: San Diego
(D) STATE OR PROVINCE: California
(E) COUNTRY: USA
(F) ZIP: 92101-3505

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/BE 96/00123

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bartfeld, Ph.D., Neil
(B) REGISTRATION NUMBER: 39,901
(C) REFERENCE/DOCKET NUMBER: VANMA83.001APC

(viii) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1429 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:181..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGGGAGCTT GGGTAGGGGC CAGGCTAGCC TGAGTGCACC CAGATGCGCT
TCTGTCAGCT 60

CTCCCTAGTG CTTCAACCAC TGCTCTCCCT GCTCTACTTT TTTTGCTCCA
GCTCAGGGAT 120

GGGGGTGGGC AGGGAAATCC TGCCACCCTC ACTTCTCCCC TTCCCATCTC
CAGGGGGGCC 180

ATG GCC AGT ACA GAG TCC TCC CTG TTG AGA TCC CTA GGC CTC AGC CCA
228

Met Ala Ser Thr Glu Ser Ser Leu Leu Arg Ser Leu Gly Leu Ser Pro
1 5 10 15

GGT CCT GGC AGC AGT GAG GTG GAG CTG GAC TGT TGG TTT GAT GAG GAT
276

Gly Pro Gly Ser Ser Glu Val Glu Leu Asp Cys Trp Phe Asp Glu Asp
20 25 30

TTC AAG TTC ATC CTG CTG CCT GTG AGC TAT GCA GTT GTC TTT GTG CTG
324

Phe Lys Phe Ile Leu Leu Pro Val Ser Tyr Ala Val Val Phe Val Leu
35 40 45

GGC TTG GGC CTT AAC GCC CCA ACC CTA TGG CTC TTC ATC TTC CGC CTC
372

Gly Leu Gly Leu Asn Ala Pro Thr Leu Trp Leu Phe Ile Phe Arg Leu
50 55 60

CGA CCC TGG GAT GCA ACG GCC ACC TAC ATG TTC CAC CTG GCA TTG TCA
420

Arg Pro Trp Asp Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser
65 70 75 80

GAC ACC TTG TAT GTG CTG TCG CTG CCC ACC CTC ATC TAC TAT TAT GCA

468

Asp Thr Leu Tyr Val Leu Ser Leu Pro Thr Leu Ile Tyr Tyr Tyr Ala

85

90

95

GCC CAC AAC CAC TGG CCC TTT GGC ACT GAG ATC TGC AAG TTC GTC CGC

516

Ala His Asn His Trp Pro Phe Gly Thr Glu Ile Cys Lys Phe Val Arg

100

105

110

TTT CTT TTC TAT TGG AAC CTC TAC TGC AGT GTC CTT TTC CTC ACC TGC

564

Phe Leu Phe Tyr Trp Asn Leu Tyr Cys Ser Val Leu Phe Leu Thr Cys

115

120

125

ATC AGC GTG CAC CGC TAC CTG GGC ATC TGC CAC CCA CTT CGG GCA CTA

612

Ile Ser Val His Arg Tyr Leu Gly Ile Cys His Pro Leu Arg Ala Leu

130

135

140

CGC TGG GGC CGC CCT CGC CTC GCA GGC CTT CTC TGC CTG GCA GTT TGG

660

Arg Trp Gly Arg Pro Arg Leu Ala Gly Leu Leu Cys Leu Ala Val Trp

145

150

155

160

TTG GTC GTA GCC GGC TGC CTC GTG CCC AAC CTG TTC TTT GTC ACA ACC

708

Leu Val Val Ala Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr

165

170

175

AGC AAC AAA GGG ACC ACC GTC CTG TGC CAT GAC ACC ACT CGG CCT GAA

756

Ser Asn Lys Gly Thr Thr Val Leu Cys His Asp Thr Thr Arg Pro Glu

180

185

190

GAG TTT GAC CAC TAT GTG CAC TTC AGC TCG GCG GTC ATG GGG CTG CTC

804

Glu Phe Asp His Tyr Val His Phe Ser Ser Ala Val Met Gly Leu Leu

195

200

205

TTT GGC GTG CCC TGC CTG GTC ACT CTT GTT TGC TAT GGA CTC ATG GCT

852

Phe Gly Val Pro Cys Leu Val Thr Leu Val Cys Tyr Gly Leu Met Ala

210

215

220

CGT CGC CTG TAT CAG CCC TTG CCA GGC TCT GCA CAG TCG TCT TCT CGC

900
 Arg Arg Leu Tyr Gln Pro Leu Pro Gly Ser Ala Gln Ser Ser Ser Arg
 225 230 235 240
 CTC CGC TCT CTC CGC ACC ATA GCT GTG GTG CTG ACT GTC TTT GCT GTC
 948
 Leu Arg Ser Leu Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val
 245 250 255
 TGC TTC GTG CCT TTC CAC ATC ACC CGC ACC ATT TAC TAC CTG GCC AGG
 996
 Cys Phe Val Pro Phe His Ile Thr Arg Thr Ile Tyr Tyr Leu Ala Arg
 260 265 270
 CTG TTG GAA GCT GAC TGC CGA GTA CTG AAC ATT GTC AAC GTG GTC TAT
 1044
 Leu Leu Glu Ala Asp Cys Arg Val Leu Asn Ile Val Asn Val Val Tyr
 275 280 285
 AAA GTG ACT CGG CCC CTG GCC AGT GCC AAC AGC TGC CTG GAT CCT GTG
 1092
 Lys Val Thr Arg Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val
 290 295 300
 CTC TAC TTG CTC ACT GGG GAC AAA TAT CGA CGT CAG CTC CGT CAG CTC
 1140
 Leu Tyr Leu Leu Thr Gly Asp Lys Tyr Arg Arg Gln Leu Arg Gln Leu
 305 310 315 320
 TGT GGT GGT GGC AAG CCC CAG CCC CGC ACG GCT GCC TCT TCC CTG GCA
 1188
 Cys Gly Gly Gly Lys Pro Gln Pro Arg Thr Ala Ala Ser Ser Leu Ala
 325 330 335
 CTA GTG TCC CTG CCT GAG GAT AGC AGC TGC AGG TGG GCG GCC ACC CCC
 1236
 Leu Val Ser Leu Pro Glu Asp Ser Ser Cys Arg Trp Ala Ala Thr Pro
 340 345 350
 CAG GAC AGT AGC TGC TCT ACT CCT AGG GCA GAT AGA TTC TAACACGGGA
 1285
 Gln Asp Ser Ser Cys Ser Thr Pro Arg Ala Asp Arg Phe
 355 360 365
 AGCCGGCAAG TGAGAGAAAA GGGGATGAGT GCAGGGCAGA GGTGAGGGAA
 CCCAATAGTG 1345

ATACCTGGTA AGGTGCTTCT TCCTCTTTTC CAGGCTCTGG AGAGAAGCCC
TCACCCTGAG 1405

GGTTGCCACG GAGGCAGGGA TATC 1429

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Ser Thr Glu Ser Ser Leu Leu Arg Ser Leu Gly Leu Ser Pro
1 5 10 15

Gly Pro Gly Ser Ser Glu Val Glu Leu Asp Cys Trp Phe Asp Glu Asp
20 25 30

Phe Lys Phe Ile Leu Leu Pro Val Ser Tyr Ala Val Val Phe Val Leu
35 40 45

Gly Leu Gly Leu Asn Ala Pro Thr Leu Trp Leu Phe Ile Phe Arg Leu
50 55 60

Arg Pro Trp Asp Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser
65 70 75 80

Asp Thr Leu Tyr Val Leu Ser Leu Pro Thr Leu Ile Tyr Tyr Tyr Ala
85 90 95

Ala His Asn His Trp Pro Phe Gly Thr Glu Ile Cys Lys Phe Val Arg
100 105 110

Phe Leu Phe Tyr Trp Asn Leu Tyr Cys Ser Val Leu Phe Leu Thr Cys
115 120 125

Ile Ser Val His Arg Tyr Leu Gly Ile Cys His Pro Leu Arg Ala Leu
130 135 140

Arg Trp Gly Arg Pro Arg Leu Ala Gly Leu Leu Cys Leu Ala Val Trp
145 150 155 160

Leu Val Val Ala Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr
165 170 175

Ser Asn Lys Gly Thr Thr Val Leu Cys His Asp Thr Thr Arg Pro Glu
180 185 190

Glu Phe Asp His Tyr Val His Phe Ser Ser Ala Val Met Gly Leu Leu
195 200 205

Phe Gly Val Pro Cys Leu Val Thr Leu Val Cys Tyr Gly Leu Met Ala
210 215 220

Arg Arg Leu Tyr Gln Pro Leu Pro Gly Ser Ala Gln Ser Ser Ser Arg
225 230 235 240

Leu Arg Ser Leu Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val
245 250 255

Cys Phe Val Pro Phe His Ile Thr Arg Thr Ile Tyr Tyr Leu Ala Arg
260 265 270

Leu Leu Glu Ala Asp Cys Arg Val Leu Asn Ile Val Asn Val Val Tyr
275 280 285

Lys Val Thr Arg Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val
290 295 300

Leu Tyr Leu Leu Thr Gly Asp Lys Tyr Arg Arg Gln Leu Arg Gln Leu
305 310 315 320

Cys Gly Gly Gly Lys Pro Gln Pro Arg Thr Ala Ala Ser Ser Leu Ala
325 330 335

Leu Val Ser Leu Pro Glu Asp Ser Ser Cys Arg Trp Ala Ala Thr Pro
340 345 350

Gln Asp Ser Ser Cys Ser Thr Pro Arg Ala Asp Arg Phe
355 360 365

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGATCTAGA TACTATGTTC TACACTCTTA CGTGC

35

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCTTAAGCTT GGAGTCACGT ACGAGCAAGC TAGTT

35